

Arndt/a

1

SEQUENCE LISTING

<110> WILSON, THOMAS G.
HEINRICH, JULIA N.

<120> RECOMBINANT BHLH-PAS/JHR POLYPEPTIDE AND ITS USE TO
SCREEN POTENTIAL INSECTICIDES

<130> 16313-0016

<140> 09/402,936

<141> 2000-01-03

<150> PCT/US98/07388

<151> 1998-04-14

<150> 08/843,205

<151> 1997-04-14

<150> 08/971,188

<151> 1997-11-17

<160> 13

<170> PatentIn Ver. 2.0

<210> 1

<211> 6234

<212> DNA

<213> Drosophila sp.

<400> 1

aggccttgac	attgtttaatc	agggtggctca	atccattata	gccatcctta	tcgaagtcga	60
tgttctcgcc	gccaaactcg	atgacctgca	aatgaatagt	gggcaaattg	tttgggatca	120
ttgaaataaa	tgactccatg	gattgagtgc	acccacctcc	ttggccctga	agggtgtccgc	180
accatggggc	actccaatga	actcgaacca	ggcccccttc	ggggggccca	gctcaccggc	240
agattgatct	ttagcttgtg	gttgtctgtg	gaactggcca	gcaaagtgga	tcccgcgacg	300
ctctccacgc	gaaccattat	gctcacgggt	tggccggaaa	actgcttcag	catgccgccc	360
ttgataatcg	agcgtggatc	aaaggcatcc	ataataactc	ctcagttaat	aacgttcaaa	420
aaacagccaa	tttcagcaga	aaatgaaatg	ccgtaaacaa	gaaagagcgc	caatagttat	480
cgagcgtgct	aatcgataat	aaaattgcat	gacgtctgct	atcgaaatta	ttcgaatttt	540
gtagcaaaaa	tatttatggg	atttattgta	acatcaaaag	ttattacatt	attactgtgg	600
acttatgtat	tataataaga	attaataaaa	ataatttata	atagaattat	aaaaagacct	660
gatagattac	atgtattaca	acaatgttat	cgacagcgaa	caagatgttc	gaatctttct	720
gatattttgt	cgggtgtgaa	cgtgcgaatt	ttagtacgac	aaccagttac	atcgatgtat	780
cgatagtttt	tagactggcc	aatgtttatt	gttataaaat	aatgtttaa	aataaacaat	840
taatcactta	gtataaacia	aaataagtgc	aagcagcaag	tgcgttggtta	aaacgaccgc	900
cgcctccga	atttccttat	tgcgggcatt	aaatcgcaac	aacaacaacg	ccaccagcaa	960
cagcaacaac	aataagcagg	agattcagat	tcgcaacgca	atcaaaacgt	aaaaaaaaaa	1020
cgaaaaataa	aaaactacia	ggcgaaacgc	ataaataaat	agggaagcaa	ataatagtaa	1080
taataagact	aaaagcaagt	ggaaaagtac	gaaagcgaaa	agagaaaaca	tatgtacgtt	1140
gcgtgagagt	gacgtgtgtg	tgtgtgtgtc	agtgcgcgaa	ggagagtgcg	cgagagaggg	1200
gaggcgagca	aaaacaaaaa	caacagcaca	gcacacagca	taagcgagac	cttgaaaact	1260
ttaaaagcag	caaaaaaac	aagacaacag	ccaaaaataa	gaaactaaaa	gctgcaaaaag	1320
taataaaaaa	tatatatttag	ccgaaaaatt	tccataataa	caattctaga	agtgcggagc	1380
gtacaccctg	ttatggagag	tgacgatttt	catttaccgc	aaggcgccaa	ttaaagggga	1440
aatccataa	atcgaggatt	acaagtggaa	aacaaggagg	cagtaactcc	agaaaacgcc	1500
caaaaagtcc	aaaatggcag	caccagagac	gggcaacacg	ggctccacag	gatccgctgg	1560

RECEIVED
02 JUN -5 PM 11:21

ctcgacagga tcgggatcgg gatcggggatc ggggaagtggg agctcctcag atccagcgaa 1620
 tggacgggag gcccgtaacc ttgccgaaaa acagcgacgg gataagctta atgccagcat 1680
 ccaggagctg gccaccatgg taccacatgc agccgaatcc tcccgtcgcc tggacaaaaac 1740
 cgccgtcctt agattcgcca cccatggcct gagacttcag tatgtctttg gcaagtccgc 1800
 ttccagacgt cgcaagaaaa ccggcctcaa gggaaacgggt atgtctgcct cacctgtcgg 1860
 agatctaccc aatcccagtc tgcattctaac ggacactcta atgcaactgc tggactgctg 1920
 cttcctcacc ctaacctgca gtggccaaat cgtttttggt tccaccagcg tggagcagct 1980
 attgggtcac tgtcagtcgg atttgtatgg ccagaatcta ctgcagatca cgcattcccg 2040
 tgatcaggat ctgttaagac agcagctaat acccagggat atagagaccc tgttctatca 2100
 gcatcagcac caccagcagc aggggcacaa tcccagcag cactccactt ccacgtcggc 2160
 ctgagcttcg ggcagtgatc tggaggagga ggaaatggag acggagggaac accgtctggg 2220
 tcggcagcag ggagaggcgg acgatgacga ggatcacccg tacaacggac gaacacccag 2280
 cccgcggaga atggcccat tggcgaccat tgatgaccga ctacgcattg atcggcgctg 2340
 ctttaccgtc cgcttggtta gggcttccac gcgagcggag gccacgcgtc attacgagcg 2400
 gggttaagatc gatggctgct ttctgcgag tgactcctcc ttaaccggag gtgcccgtgc 2460
 caactatccg attgtctccc agctgatacg acgtcgcaga aacaacaata tgctggctgc 2520
 cgctgcagca gtggcagcag aagcggcgac ggtgccaccc cagcagcatg ccattgccc 2580
 ggcggcgctg cacgggatta gcggcaatga tattgtcctg gtggccatgg ccagggtgct 2640
 gcgagaggaa cggccgcctg aggagacgga gggtagagt ggcttgacca tttacagaca 2700
 gccagaaccc tatcagctgg agtaccatac gaggcattcta atcgacggca gcatcatcga 2760
 ctgtgatcaa aggattggc tgggtggcgg atatatgaag gatgaggtgg gtatatatac 2820
 atcatctctc tgaactgctt acgacaacta atcgtgtact ctccactcga aacagggtgcg 2880
 caaccttagt cctttctgtt tcatgcacct ggacgacgtt cgctgggtga ttgtggccct 2940
 tcgacaaatg tacgattgca acagtgacta tggcgagagc tgctaccgtc tgctgtccc 3000
 caacgggcgc ttcatttacc tgcacaccaa gggatttctg gaggtcgacc gtggcagtaa 3060
 taagggtgat tcttttctgt gcgtcaacac gctgctcgat gaggaggcgg gccggcaaaa 3120
 ggtgcaggag atgaaggaga aattctcgac aatcatcaag gcggagatgc ccacgcagag 3180
 cagcagtcct gatttgccc cctcgcaggc accgcagcaa cttgagagaa ttgtcctcta 3240
 tctaatagag aacctacaga agagtgtgga ttcagcagag acggttgggc gccagggcat 3300
 ggaaagccta atggacgatg gctacagtct gccagcaaat accttaactc tcgaggagtt 3360
 agtccctcgc cccacgccc ccttggcctt ggtgcgcgcg gctccctcat cgggtcaagag 3420
 ctccatctcc aagtccgtga gtgtggtcaa tgtgacggcg gccagaaagt ttcagcagga 3480
 gcatcagaag cagcgtgaac gtgaccgtga gcagcttaag gagcgcacca actccacgca 3540
 gggcgtgatc cggcaactga gcagctgcct aagcagggcg gaaacggcat cctgtatcct 3600
 atcaccagcc agtagcttga gtgccagcga agcaccggac acgcccgatc cgcacagcaa 3660
 cacatcaccg ccaccgtcgc tccacacacg tcccagtgct ctgcatcgaa ccctgaccag 3720
 cagctgcga tgacgggctg atggaacctg gtttgccttc taattgggtg tgtggaaatg 3780
 gacgtaattg gtagctcacg tgcccacaaa cgaattagta tcggtaatat aatcctggcc 3840
 aatcgcaatg tgaaaaccca aaatgtatca gaaaaaaaac gagcattatt caaatagttt 3900
 aaaaattcag ccaaaaaact taaatacgaa aaaaaagagc gtgggttgaa gaaccttttg 3960
 ttttcatatt cacatttcca agctttgagc aatcaaaaaa ttttaatttt cagtatacac 4020
 atatgtataa tgagttggct ttacaaaagc tattaacaaa tcaagcaatt gtgtaattta 4080
 atatgagact ttccgtgatt tttgctttct acgtactttt cgacttcaat tgatctatag 4140
 ggtttccgta ttaaaaacga aattaacgtg gtttcatatt atgaaaatgc aatatgagct 4200
 cgcatttatt ttgatattat gacagtaata atgatctgat cacgataatc gttttctcaa 4260
 aacataagcg atacattttg ggtacatttg gccattactg tttctgtgtg tgatttcgg 4320
 ataaaatagt agtttgatta catgttatat tgatgaatgg cgatcgggtg gtgctgctaa 4380
 atgcgttcca ttatcaataa ttttcggtat gtaattacgt ttaatttgta aatatgtatg 4440
 agtgcgagcg tgagtgagtt tgtgatcgtg tcagcatggg tgtgaatgaa cattagatca 4500
 gtgctcggat ttggtttttag ttgaaattta aaccccatth ccccgatttc ccagttatca 4560
 ccttccgccc caaaacacca ttgtaaaaag agtacaaaaa aaaaaaaaaa agaaaataga 4620
 aaaacaaaca aacaattata tatttatttc gccctaagtc tagaacgtgc taaacacaac 4680
 tcattaatag ttaaacaaac ggatgttgca atcgatggaa attaaacgct cgcttttagt 4740
 tttgccgtct cgctcgaaga aagaaagagg actactacat atgtacagtc aaactaatcc 4800
 aagtcaaact cttcagctctc agaattggag actttattaa aggtttttta ttttatgaag 4860
 aatagcatat tattttttata tatatatatt tatgtatata tatttatatc acaaatctcc 4920
 ttcgatatcc ctttgtaatc tataaaaaaca cttccaggcg cagctttatt tttcaacagt 4980
 ttttaattttg ggaactttac aaagcatata agcatacccc aaatccatat ccttataaac 5040

tttgtagtta ttacaaatgt gttcaaaatt aaaaaaaaaa aagtttgtca tccaaaatcc 5100
 aatccgctaa atacaatata atcattttta ttgatctatg ttacacttct ataattgtcta 5160
 ctggacaaaa tatgattaag ttgaaatttc aaagtgtttt tgaagtttgt actaacgaag 5220
 tttggctgta gttcaatact cacagaaagg gagcgagaca tattcccatc tcgctccgac 5280
 ctgttatcaa agccttttgc attgtccttg gcgttgcgtt cttatcaccc gcgtatcgga 5340
 gggaatatat gatttttttt tcggccaagt ggttctagt gtaaatatga agcgggtgggt 5400
 gggttccggg gggttggggg aaccgcggtt ggtgatgggc gcagagaagg cgggaagcgg 5460
 gggggaacac gtttcgttat tttttgtttt atagcgaaat tcctctagct ataatgtat 5520
 gcatacatat atgctattaa cttttcgttt agctcaattt tttgtttgta tttttaatta 5580
 taactcgggt tgtctagtgt gtaattaaat taaaagtcca atgctaattc cccagcgaat 5640
 cgttcagtgt ttgttcaaac gagttgtgct ctttaaacac ttttggctta tcctttcatt 5700
 taatttttgt ttgttttcct tgcgttggtt tatgtccaaa taaaaatgaa agtttgaatt 5760
 gttttttttt agtaatttag ttttaactgt aatgtcaaat gtcgagaggt atactctgta 5820
 taagaataat aatgtgtaat gtaattttta gaacttgcta atctctagca attaaaacat 5880
 agcctgtaat taacaataat taattataat aaccagtaac agttcatgca aatgaaacct 5940
 taataaataa taaattatat aaaagaagat ggaagtgttt tcaatcaatg aagttacttc 6000
 ctattttcag gagttggaat gttacacttt tttataagct gatttgaaat gcgcgccaca 6060
 ttatatctgc cttgcgcgca cgcattgcag ccgaataacg gcgaattaac tccctcaga 6120
 ggtgagtttg aactatcgat tataatcgat tgcattcgga aacaaaaaac accttgagtt 6180
 tggtcagatc gggttttgcgc gggataaata ataaaatatt aaatgttttc tttg 6234

<210> 2

<211> 3011

<212> DNA

<213> *Drosophila* sp.

<400> 2

ccaaaaataa gaaactaaaa gctgcaaaag taataaaaaa tatatttttag ccgaaaaatt 60
 tccataataa caattctaga agtgccgagc gtacaccctg ttatggagag tgacgatttt 120
 catttaccgc aaggcgccaa ttaaagggga aaatccataa atcgaggatt acaagtggaa 180
 aacaaggagg cagtaactcc agaaaacgcc caaaaagtcc aaaatggcag caccagagac 240
 gggcaacacg ggctccacag gatccgctgg ctcgacagga tcgggatcgg gatcgggac 300
 gggaagtggg agctcctcag atccagcgaa tggacgggag gcccgtaacc ttgccgaaaa 360
 acagcgacgg gataagctta atgccagcat ccaggagctg gccaccatgg taccacatgc 420
 agccgaatcc tcccgtcgcc tggacaaaac cgccgtcctt agattcgcca cccatggcct 480
 gagacttcag tatgtctttg gcaagtccgc ttccagacgt cgcaagaaaa ccggcctcaa 540
 gggaacgggt atgtctgcct cacctgtcgg agatctaccc aatcccagtc tgcactaac 600
 ggacactcta atgcaactgc tggactgctg ctctctcacc ctaacctgca gtggccaaat 660
 cgttttggta tccaccagcg tggagcagct attgggtcac tgtcagtcgg atttgtatgg 720
 ccagaatcta ctgcagatca cgcacccga tgatcaggat ctgttaagac agcagctaatt 780
 acccagggat atagagaccc tgttctatca gcatcagcac caccagcagc aggggcacaa 840
 tccccagcag cactccactt ccacgtcggc ctcarcttcg ggcagtgate tggaggagga 900
 ggaaatggag acggagggaac accgtctggg tcggcagcag ggagaggcgg acgatgacga 960
 ggatcacccg tacaaccgac gaacacccag ccgcgggaga atggccatt tggcgacct 1020
 tgatgaccga ctacgcattg atcggcgctg ctttaccgtc cgcttggtta gggcttccac 1080
 gcgagcggag gccacgcgtc attacgagcg ggttaagatc gatggctgct ttcgtcgcag 1140
 tgactcctcc ttaaccggag gtgccgctgc caactatccg attgtctccc agctgatacg 1200
 acgctcgaga aacaacaata tgcctggctg tgcctgcagca gtggcagcag aagcggcgac 1260
 ggtgccgccc cagcacgatg ccattgccca ggcggcgctg cacgggatta gcggcaatga 1320
 tattgtcctg gtggccatgg ccagggtgct gcgagaggaa cggccgctg aggagacgga 1380
 gggtagagtg ggcttgacca tttacagaca gccagaaccc tatcagttgg agtaccatac 1440
 gaggcattcta atcgacggca gcatcatcga ctgtgatcaa aggattggct tgggtggcgg 1500
 atatataaag gatgaggtgg gtatattaac atcatctctc tgaactgctt acgacaacta 1560
 atcgtgtact ctccactcga aacagggtgc caaccttagt cccttctggt tcatgcacct 1620
 ggacgacgtt cgctgggtga ttgtggcctt tcgacaaatg tacgattgca acagtgacta 1680
 cggcgagagc tgctaccgtc tgcgtgtccc caacgggcgc ttcatttacc tgcacaccaa 1740
 gggattttct gaggtcgacc gtggcagtaa taagggtgat tcctttctgt gcgtcaacac 1800
 gctgctcgat gaggaggcgg gccggcaaaa ggtgcaggag atgaaggaga aattctcgac 1860

aatcatcaag	gcggagatgc	ccacgcagag	cagcagtccc	gatttgcccg	cctcgcaggc	1920
accgcagcaa	cttgagagaa	ttgtcctcta	tctaatagag	aacctacaga	agagtgtgga	1980
ttcagcagag	acggttggcg	gccagggcat	ggaaagccta	atggacgatg	gctacagttc	2040
gccagcaaat	accttaactc	tcgaggagtt	agctccctcg	cccacgcccg	ccttggcctt	2100
ggtgccgccg	gctccctcat	cggccaagag	ctccatctcc	aagtcggtga	gtgtggtcaa	2160
tgtgacggcg	gccagaaagt	ttcagcagga	gcatacagaag	cagcgtgaac	gtgaccgtga	2220
gcagcttaag	gagcgcacca	actccacgca	gggcgtgatc	cggcaactga	gcagctgcct	2280
aagcgaggcg	gaaacggcat	cctgtatcct	atcaccagcc	agtagcttga	gtgccagcga	2340
agcaccggac	acgcccgatc	cgcacagcaa	cacatcacccg	ccaccgtcgc	tccacacacg	2400
tcccagtgtc	ctgcatacga	ccctgaccag	cacgctgcga	tgacgggctg	atggaacctg	2460
gtttgccttc	taattgggtg	tgtggaaatg	gacgtaattg	gtagctcacg	tgcccacaaa	2520
cgaattagta	tcggtaatat	aatcctggcc	aatcgcaatg	tgaaaaccca	aaatgtatca	2580
gaaaaaaaaac	gagcattatt	caaatagttt	aaaaattcag	ccaaaaaact	taaaaacgaa	2640
aaaaaagagc	gtgggttgaa	gaaccttttg	ttttcatatt	cacattttcca	agctttgagc	2700
aatcaaacia	ttttaatttt	cagtatacac	atatgtataa	tgagttggct	ttacaaaagc	2760
tattaacaaa	tcaagcaatt	gtgtaattta	atatgagact	ttccgtgatt	tttgctttct	2820
acgtactttt	cgacttcaat	tgatctatag	ggtttccgta	ttaaaaacga	aattaacgtg	2880
gtttcatttg	atgaaaatgc	aatatgagct	cgcattttatt	ttgatattat	gacagtaata	2940
atgatctgat	cacgataatc	gttttctcaa	aacataagcg	atacattttg	ggtacatttg	3000
gccattactg	t					3011

<210> 3

<211> 3282

<212> DNA

<213> *Drosophila* sp.

<400> 3

aaataagaaa	ctaaaagctg	caaaagtaat	aaaaaatata	ttttagccga	aaaattttcca	60
taataacaat	tctagaagtg	cggagcgtac	accctgttat	ggagagtgc	gatttttcatt	120
taccgcaagg	cgccaattaa	aggggaaaat	ccataaatcg	aggattacaa	gtggaaaaca	180
aggaggcagt	aactccagaa	aacgcccana	aagtccaaaa	tggcagcacc	agagacgggc	240
aacacgggct	ccacaggatc	cgtcggtcgc	acaggatcgc	gatcgggatc	gggatcggga	300
agtgggagct	cctcagatcc	agcgaatgga	cgggaggccc	gtaaccttgc	cgaaaaacag	360
cgacgggata	agcttaatgc	cagcatccag	gagctggcta	ccatgggtacc	acatgcagcc	420
gaatcctccc	gtcgcctgga	caaaaccgcc	gtcctcagat	ttgccaccca	tggcctgaga	480
cttcagtatg	tctttggcaa	gtccgcttcc	agacgtcgca	agaaamccgg	cctcaaggga	540
acgggtatgt	ctgcctcacc	tgtcggagat	ctacccaatc	ccagtctgca	tctaacggac	600
actctaattgc	aactgctgga	ctgctgcttc	ctcacccata	cctgcagtgg	ccaaatcggt	660
ttggtatcca	ccagcgtgga	gcagctattg	ggtcactgtc	agtccgattt	gtatggccag	720
aatctactgc	agatcacgca	tcccgatgat	caggatctgt	taagacagca	gctaataccc	780
agggatatag	agaccctggt	ctatcagcat	cagcaccacc	agcagcaggg	gcacaatccc	840
cagcagcact	ccacttccac	gtcggcctca	gcttcgggca	gtgatctgga	ggaggaggaa	900
atggagacgg	aggaacaccg	tctgggtcgg	cagcagggag	aggcggacga	tgacgaggat	960
caccgcgtaca	accgacgaac	acccagcccg	cggagaatgg	cccatttggc	gaccattgat	1020
gaccgactac	gcatggattg	gcgctgcttt	accgtccgct	tggctagggc	ttccacgcga	1080
gcggaggcca	cgcgtcatta	cgagcggggt	aagatcgatg	gctgctttcg	tcgcagtgc	1140
tcctccttaa	ccggagggtgc	cgtcgccaac	tatccgattg	tctcccagct	gatacgacgc	1200
tcgagaaaca	acaatatgct	ggctgccgct	gcagcagtgg	cagcagaagc	ggcgacgggtg	1260
ccaccccagc	acgatgccat	tgcccaggcg	gcgctgcacg	ggattagcgg	caatgatatt	1320
gtcctgggtg	ccatggccag	gggtgctgcga	gaggaacggc	cgcctgagga	gacggagggt	1380
acagtgggct	tgaccattta	cagacagcca	gaacctatc	agctggagta	ccatacgagg	1440
catctaattcg	acggcagcat	catcgactgt	gatcaaagga	ttggtctggt	ggcgggatat	1500
atgaaggatg	aggtgcgcaa	ccttagtccc	ttctgtttca	tgcacctgga	cgacgttcgc	1560
tgggtgattg	tggcccttcg	acaaatgtac	gattgcaaca	gtgactatgg	cgagagctgc	1620
taccgtctgc	tgtcccgcga	cgggcgcttc	atttacctgc	acaccaaggg	atttctggag	1680
gtcgaccgtg	gcagtaataa	gggtgcattcc	tttctgtgcg	tcaacacgct	gctcgatgag	1740
gaggcggggc	ggcaaaaggt	gcaggagatg	aaggagaaat	tctcgacaat	catcaaggcg	1800

gagatgccca cgcagagcag cagtcccgat ttgcccgcct cgcaggcacc gcagcaactt 1860
 gagagaattg tcctctatct aatagagaac ctacagaaga gtgtggattc agcagagacg 1920
 gttggcggcc agggcatgga aagcctaattg gacgatggct acagttcgcc agcaaatacc 1980
 ttaactctcg aggagttagc tccctcgccc acgcccgcct tggccttggt gccgccggct 2040
 ccctcatcgg tcaagagctc catctccaag tcggtgagtg tggccaatgt gacggcggcc 2100
 agaaagtttc agcaggagca tcagaagcag cgtgaacgtg accgtgagca gcttaaggag 2160
 cgcaccaact ccacgcaggg cgtgatccgg caactgagca gctgcctaag cgaggcggaa 2220
 acggcatcct gtatcctatc accagccagt agcttgagtg ccagcgaagc accggacacg 2280
 cccgatccgc acagcaacac atcaccgcca ccgtcgctcc acacacgtcc cagtgtcctg 2340
 catcgaaccc tgaccagcac gctgcgatga cgggctgatg gaacctgggt tgccttctaa 2400
 ttgggtgtgt ggaaatggac gtaattggta gctcacgtgc ccacaaacga attagtatcg 2460
 gtaatatataat cctggccaat cgcaatgtga aaacccaaaaa tgtatcagaa aaaaaacgag 2520
 cattattcaa atagtttaaa aattcagcca aaaaacttaa aaacgaaaaa aaagagcgtg 2580
 ggttgaagaa ccttttggtt tcatattcac atttccaagc tttgagcaat caaacaattt 2640
 taattttcag tatacacata tgtataatga gttggcttta caaaagctat taacaaatca 2700
 agcaattgtg taatttaata tgagactttc cgtgattttt gctttctacg tacttttcga 2760
 cttcaattga tctatagggt ttcctgatta aaaacgaaat taacgtgggt tcattttgatg 2820
 aaaatgcaat atgagctcgc atttattttg atattatgac agtaataatg atctgatcac 2880
 gataatcggt ttctcaaaac ataagcgata cattttgggt acatttggcc attactgttt 2940
 ctgtgtgtga ttctcggtata aaatagtagt ttgattacat gttatattga tgaatggcga 3000
 tcggtgggtg ctgctaaatg cgttccatta tcaataattt tcgttatgta attacgttta 3060
 atttgtaa atgtatgagt gcgagcgtga gtgagtttgt gatcgtgtca gcatgggtgt 3120
 gaatgaacat tagatcagtg ctcggatttg gtttttagttg aaatttaaac cccatttccc 3180
 cgatttccca gttatcacct tccgccccaa aacaccattg taaaaagagt acaaaaaaaaa 3240
 aaagaaaaga aaatagaaaa acaaaaaaaaaa aaaaaaaaaa aa 3282

<210> 4
 <211> 737
 <212> PRT
 <213> Drosophila sp.

<220>
 <221> MOD_RES
 <222> (218)
 <223> Thr or Pro

<400> 4
 Met Ala Ala Pro Glu Thr Gly Asn Thr Gly Ser Thr Gly Ser Ala Gly
 1 5 10 15
 Ser Thr Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser Ser Ser
 20 25 30
 Asp Pro Ala Asn Gly Arg Glu Ala Arg Asn Leu Ala Glu Lys Gln Arg
 35 40 45
 Arg Asp Lys Leu Asn Ala Ser Ile Gln Glu Leu Ala Thr Met Val Pro
 50 55 60
 His Ala Ala Glu Ser Ser Arg Arg Leu Asp Lys Thr Ala Val Leu Arg
 65 70 75 80
 Phe Ala Thr His Gly Leu Arg Leu Gln Tyr Val Phe Gly Lys Ser Ala
 85 90 95
 Ser Arg Arg Arg Lys Lys Thr Gly Leu Lys Gly Thr Gly Met Ser Ala
 100 105 110

Ser	Pro	Val	Gly	Asp	Leu	Pro	Asn	Pro	Ser	Leu	His	Leu	Thr	Asp	Thr	115	120	125
Leu	Met	Gln	Leu	Leu	Asp	Cys	Cys	Phe	Leu	Thr	Leu	Thr	Cys	Ser	Gly	130	135	140
Gln	Ile	Val	Leu	Val	Ser	Thr	Ser	Val	Glu	Gln	Leu	Leu	Gly	His	Cys	145	150	155
Gln	Ser	Asp	Leu	Tyr	Gly	Gln	Asn	Leu	Leu	Gln	Ile	Thr	His	Pro	Asp	165	170	175
Asp	Gln	Asp	Leu	Leu	Arg	Gln	Gln	Leu	Ile	Pro	Arg	Asp	Ile	Glu	Thr	180	185	190
Leu	Phe	Tyr	Gln	His	Gln	His	His	Gln	Gln	Gln	Gly	His	Asn	Pro	Gln	195	200	205
Gln	His	Ser	Thr	Ser	Thr	Ser	Ala	Ser	Xaa	Ser	Gly	Ser	Asp	Leu	Glu	210	215	220
Glu	Glu	Glu	Met	Glu	Thr	Glu	Glu	His	Arg	Leu	Gly	Arg	Gln	Gln	Gly	225	230	235
Glu	Ala	Asp	Asp	Asp	Glu	Asp	His	Pro	Tyr	Asn	Arg	Arg	Thr	Pro	Ser	245	250	255
Pro	Arg	Arg	Met	Ala	His	Leu	Ala	Thr	Ile	Asp	Asp	Arg	Leu	Arg	Met	260	265	270
Asp	Arg	Arg	Cys	Phe	Thr	Val	Arg	Leu	Ala	Arg	Ala	Ser	Thr	Arg	Ala	275	280	285
Glu	Ala	Thr	Arg	His	Tyr	Glu	Arg	Val	Lys	Ile	Asp	Gly	Cys	Phe	Arg	290	295	300
Arg	Ser	Asp	Ser	Ser	Leu	Thr	Gly	Gly	Ala	Ala	Ala	Asn	Tyr	Pro	Ile	305	310	315
Val	Ser	Gln	Leu	Ile	Arg	Arg	Ser	Arg	Asn	Asn	Asn	Met	Leu	Ala	Ala	325	330	335
Ala	Ala	Ala	Val	Ala	Ala	Glu	Ala	Ala	Thr	Val	Pro	Pro	Gln	His	Asp	340	345	350
Ala	Ile	Ala	Gln	Ala	Ala	Leu	His	Gly	Ile	Ser	Gly	Asn	Asp	Ile	Val	355	360	365
Leu	Val	Ala	Met	Ala	Arg	Val	Leu	Arg	Glu	Glu	Arg	Pro	Pro	Glu	Glu	370	375	380
Thr	Glu	Gly	Thr	Val	Gly	Leu	Thr	Ile	Tyr	Arg	Gln	Pro	Glu	Pro	Tyr	385	390	395
Gln	Leu	Glu	Tyr	His	Thr	Arg	His	Leu	Ile	Asp	Gly	Ser	Ile	Ile	Asp	405	410	415

Cys Asp Gln Arg Ile Gly Leu Val Ala Gly Tyr Met Lys Asp Glu Val
 420 425 430
 Gly Ile Leu Thr Ser Ser Leu Thr Ala Tyr Asp Asn Ser Cys Thr Leu
 435 440 445
 His Ser Lys Gln Val Arg Asn Leu Ser Pro Phe Cys Phe Met His Leu
 450 455 460
 Asp Asp Val Arg Trp Val Ile Val Ala Leu Arg Gln Met Tyr Asp Cys
 465 470 475 480
 Asn Ser Asp Tyr Gly Glu Ser Cys Tyr Arg Leu Leu Ser Arg Asn Gly
 485 490 495
 Arg Phe Ile Tyr Leu His Thr Lys Gly Phe Leu Glu Val Asp Arg Gly
 500 505 510
 Ser Asn Lys Val His Ser Phe Leu Cys Val Asn Thr Leu Leu Asp Glu
 515 520 525
 Glu Ala Gly Arg Gln Lys Val Gln Glu Met Lys Glu Lys Phe Ser Thr
 530 535 540
 Ile Ile Lys Ala Glu Met Pro Thr Gln Ser Ser Ser Pro Asp Leu Pro
 545 550 555 560
 Ala Ser Gln Ala Pro Gln Gln Leu Glu Arg Ile Val Leu Tyr Leu Ile
 565 570 575
 Glu Asn Leu Gln Lys Ser Val Asp Ser Ala Glu Thr Val Gly Gly Gln
 580 585 590
 Gly Met Glu Ser Leu Met Asp Asp Gly Tyr Ser Ser Pro Ala Asn Thr
 595 600 605
 Leu Thr Leu Glu Glu Leu Ala Pro Ser Pro Thr Pro Ala Leu Ala Leu
 610 615 620
 Val Pro Pro Ala Pro Ser Ser Val Lys Ser Ser Ile Ser Lys Ser Val
 625 630 635 640
 Ser Val Val Asn Val Thr Ala Ala Arg Lys Phe Gln Gln Glu His Gln
 645 650 655
 Lys Gln Arg Glu Arg Asp Arg Glu Gln Leu Lys Glu Arg Thr Asn Ser
 660 665 670
 Thr Gln Gly Val Ile Arg Gln Leu Ser Ser Cys Leu Ser Glu Ala Glu
 675 680 685
 Thr Ala Ser Cys Ile Leu Ser Pro Ala Ser Ser Leu Ser Ala Ser Glu
 690 695 700
 Ala Pro Asp Thr Pro Asp Pro His Ser Asn Thr Ser Pro Pro Pro Ser
 705 710 715 720

```
<210> 5
<211> 716
<212> PRT
<213> Drosophila sp.
```

```
<220>
<221> MOD_RES
<222> (103)
<223> Gly or Arg
```

```

<400> 5
Met Ala Ala Pro Glu Thr Gly Asn Thr Gly Ser Thr Gly Ser Ala Gly
  1          5          10          15

Ser Thr Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser Ser Ser
      20          25          30

Asp Pro Ala Asn Gly Arg Glu Ala Arg Asn Leu Ala Glu Lys Gln Arg
      35          40          45

Arg Asp Lys Leu Asn Ala Ser Ile Gln Glu Leu Ala Thr Met Val Pro
      50          55          60

His Ala Ala Glu Ser Ser Arg Arg Leu Asp Lys Thr Ala Val Leu Arg
      65          70          75          80

Phe Ala Thr His Gly Leu Arg Leu Gln Tyr Val Phe Gly Lys Ser Ala
      85          90          95

Ser Arg Arg Arg Lys Lys Xaa Gly Leu Lys Gly Thr Gly Met Ser Ala
      100          105          110

Ser Pro Val Gly Asp Leu Pro Asn Pro Ser Leu His Leu Thr Asp Thr
      115          120          125

Leu Met Gln Leu Leu Asp Cys Cys Phe Leu Thr Leu Thr Cys Ser Gly
      130          135          140

Gln Ile Val Leu Val Ser Thr Ser Val Glu Gln Leu Leu Gly His Cys
      145          150          155          160

Gln Ser Asp Leu Tyr Gly Gln Asn Leu Leu Gln Ile Thr His Pro Asp
      165          170          175

Asp Gln Asp Leu Leu Arg Gln Gln Leu Ile Pro Arg Asp Ile Glu Thr
      180          185          190

Leu Phe Tyr Gln His Gln His His Gln Gln Gln Gly His Asn Pro Gln
      195          200          205

Gln His Ser Thr Ser Thr Ser Ala Ser Ala Ser Gly Ser Asp Leu Glu
      210          215          220

```


Glu Glu Glu Met Glu Thr Glu Glu His Arg Leu Gly Arg Gln Gln Gly
 225 230 235 240
 Glu Ala Asp Asp Asp Glu Asp His Pro Tyr Asn Arg Arg Thr Pro Ser
 245 250 255
 Pro Arg Arg Met Ala His Leu Ala Thr Ile Asp Asp Arg Leu Arg Met
 260 265 270
 Asp Trp Arg Cys Phe Thr Val Arg Leu Ala Arg Ala Ser Thr Arg Ala
 275 280 285
 Glu Ala Thr Arg His Tyr Glu Arg Val Lys Ile Asp Gly Cys Phe Arg
 290 295 300
 Arg Ser Asp Ser Ser Leu Thr Gly Gly Ala Ala Ala Asn Tyr Pro Ile
 305 310 315 320
 Val Ser Gln Leu Ile Arg Arg Ser Arg Asn Asn Asn Met Leu Ala Ala
 325 330 335
 Ala Ala Ala Val Ala Ala Glu Ala Ala Thr Val Pro Pro Gln His Asp
 340 345 350
 Ala Ile Ala Gln Ala Ala Leu His Gly Ile Ser Gly Asn Asp Ile Val
 355 360 365
 Leu Val Ala Met Ala Arg Val Leu Arg Glu Glu Arg Pro Pro Glu Glu
 370 375 380
 Thr Glu Gly Thr Val Gly Leu Thr Ile Tyr Arg Gln Pro Glu Pro Tyr
 385 390 395 400
 Gln Leu Glu Tyr His Thr Arg His Leu Ile Asp Gly Ser Ile Ile Asp
 405 410 415
 Cys Asp Gln Arg Ile Gly Leu Val Ala Gly Tyr Met Lys Asp Glu Val
 420 425 430
 Arg Asn Leu Ser Pro Phe Cys Phe Met His Leu Asp Asp Val Arg Trp
 435 440 445
 Val Ile Val Ala Leu Arg Gln Met Tyr Asp Cys Asn Ser Asp Tyr Gly
 450 455 460
 Glu Ser Cys Tyr Arg Leu Leu Ser Arg Asn Gly Arg Phe Ile Tyr Leu
 465 470 475 480
 His Thr Lys Gly Phe Leu Glu Val Asp Arg Gly Ser Asn Lys Val His
 485 490 495
 Ser Phe Leu Cys Val Asn Thr Leu Leu Asp Glu Glu Ala Gly Arg Gln
 500 505 510
 Lys Val Gln Glu Met Lys Glu Lys Phe Ser Thr Ile Ile Lys Ala Glu
 515 520 525

Met Pro Thr Gln Ser Ser Ser Pro Asp Leu Pro Ala Ser Gln Ala Pro
530 535 540

Gln Gln Leu Glu Arg Ile Val Leu Tyr Leu Ile Glu Asn Leu Gln Lys
545 550 555 560

Ser Val Asp Ser Ala Glu Thr Val Gly Gly Gln Gly Met Glu Ser Leu
565 570 575

Met Asp Asp Gly Tyr Ser Ser Pro Ala Asn Thr Leu Thr Leu Glu Glu
580 585 590

Leu Ala Pro Ser Pro Thr Pro Ala Leu Ala Leu Val Pro Pro Ala Pro
595 600 605

Ser Ser Val Lys Ser Ser Ile Ser Lys Ser Val Ser Val Val Asn Val
610 615 620

Thr Ala Ala Arg Lys Phe Gln Gln Glu His Gln Lys Gln Arg Glu Arg
625 630 635 640

Asp Arg Glu Gln Leu Lys Glu Arg Thr Asn Ser Thr Gln Gly Val Ile
645 650 655

Arg Gln Leu Ser Ser Cys Leu Ser Glu Ala Glu Thr Ala Ser Cys Ile
660 665 670

Leu Ser Pro Ala Ser Ser Leu Ser Ala Ser Glu Ala Pro Asp Thr Pro
675 680 685

Asp Pro His Ser Asn Thr Ser Pro Pro Pro Ser Leu His Thr Arg Pro
690 695 700

Ser Val Leu His Arg Thr Leu Thr Ser Thr Leu Arg
705 710 715

<210> 6
<211> 250
<212> DNA
<213> *Drosophila melanogaster*

<400> 6
atggcagcac cagagacggg caacacgggc tccacaggat ccgctggctc gacaggatcg 60
ggatcgggat cgggatcggg aagtgggagc tcctcagatc cagcgaatgg acgggaggcc 120
cgtaaccttg ccgaaaaaca gcgacgggat aagcttaatg ccagcatcca ggagctggct 180
accatggtac cacatgcagc cgaatcctcc cgtcgcctgg acaaaaccgc cgtccttaga 240
ttcgccaccc 250

<210> 7
<211> 232
<212> DNA
<213> *Drosophila erecta*

<400> 7
cagcagacgc gggcaacacg ggcaccacag gatcagctgg gtccacagga tcgggatcgg 60
gaactgggac gtccgcagat ccagcgaatg gacgggaggc ccgcaatctt gccgagaaac 120
agcgacggga taagcttaat gccagcatcc aggagctggc taccatggta ccacatgtca 180

gccgaatcct cccgacgcct ggacaaaacc gccgtcctca gattcgccac cc

232

<210> 8

<211> 631

<212> PRT

<213> Drosophila sp.

<400> 8

Met Asp Glu Ala Asn Ile Gln Asp Lys Glu Arg Phe Ala Ser Arg Glu
1 5 10 15

Asn His Cys Glu Ile Glu Arg Arg Arg Asn Lys Met Thr Ala Tyr
20 25 30

Ile Thr Glu Leu Ser Asp Met Val Pro Thr Cys Ser Ala Leu Ala Arg
35 40 45

Lys Pro Asp Lys Leu Thr Ile Leu Arg Met Ala Val Ala His Met Lys
50 55 60

Ala Leu Arg Gly Thr Gly Asn Thr Ser Ser Asp Gly Thr Tyr Lys Pro
65 70 75 80

Ser Phe Leu Thr Asp Gln Glu Leu Lys His Leu Ile Leu Glu Ala Ala
85 90 95

Asp Gly Phe Leu Phe Val Val Ser Cys Asp Ser Gly Arg Val Ile Tyr
100 105 110

Val Ser Asp Ser Val Thr Pro Val Leu Asn Tyr Thr Gln Ser Asp Trp
115 120 125

Tyr Gly Thr Ser Leu Tyr Glu His Ile His Pro Asp Asp Arg Glu Lys
130 135 140

Ile Arg Glu Gln Leu Ser Thr Gln Glu Ser Gln Asn Ala Gly Arg Ile
145 150 155 160

Leu Asp Leu Lys Ser Gly Thr Val Lys Lys Glu Gly His Gln Ser Ser
165 170 175

Met Arg Leu Ser Met Gly Ala Arg Arg Gly Phe Ile Cys Met Arg Val
180 185 190

Gly Asn Val Asn Pro Glu Ser Met Val Ser Gly His Leu Asn Arg Leu
195 200 205

Lys Gln Arg Asn Ser Leu Gly Pro Ser Arg Asp Gly Thr Asn Tyr Ala
210 215 220

Val Val His Cys Thr Gly Tyr Ile Lys Asn Trp Pro Pro Thr Asp Met
225 230 235 240

Phe Pro Asn Met His Met Glu Arg Asp Val Asp Asp Met Ser Ser His
245 250 255

Cys	Cys	Leu	Val	Ala	Ile	Gly	Arg	Leu	Gln	Val	Thr	Ser	Thr	Ala	Ala	260	265	270
Asn	Asp	Met	Ser	Gly	Ser	Asn	Asn	Gln	Ser	Glu	Phe	Ile	Thr	Arg	His	275	280	285
Ala	Met	Asp	Gly	Lys	Phe	Thr	Phe	Val	Asp	Gln	Arg	Val	Leu	Asn	Ile	290	295	300
Leu	Gly	Tyr	Thr	Pro	Thr	Glu	Leu	Leu	Gly	Lys	Ile	Cys	Tyr	Asp	Phe	305	310	315
Phe	His	Pro	Glu	Asp	Gln	Ser	His	Met	Lys	Glu	Ser	Phe	Asp	Gln	Val	325	330	335
Leu	Lys	Gln	Lys	Gly	Gln	Met	Phe	Ser	Leu	Leu	Tyr	Arg	Ala	Arg	Ala	340	345	350
Lys	Asn	Ser	Glu	Tyr	Tyr	Val	Trp	Leu	Arg	Thr	Gln	Ala	Tyr	Ala	Phe	355	360	365
Leu	Asn	Pro	Tyr	Thr	Asp	Glu	Val	Glu	Tyr	Ile	Val	Cys	Thr	Asn	Ser	370	375	380
Ser	Gly	Lys	Thr	Met	His	Gly	Ala	Pro	Leu	Asp	Ala	Ala	Ala	Ala	His	385	390	395
Thr	Pro	Glu	Gln	Val	Gln	Gln	Gln	Gln	Gln	Gln	Gln	Gln	Glu	Gln	His	405	410	415
Val	Tyr	Val	Gln	Ala	Ala	Pro	Gly	Val	Asp	Tyr	Ala	Arg	Arg	Glu	Leu	420	425	430
Thr	Pro	Val	Gly	Ser	Ala	Thr	Asn	Asp	Gly	Met	Tyr	Gln	Thr	His	Met	435	440	445
Leu	Ala	Met	Gln	Ala	Pro	Thr	Pro	Gln	Gln	Gln	Gln	Gln	Gln	Gln	Gln	450	455	460
Arg	Pro	Gly	Ser	Ala	Gln	Thr	Thr	Pro	Val	Gly	Tyr	Thr	Tyr	Asp	Thr	465	470	475
Thr	His	Ser	Pro	Tyr	Ser	Ala	Gly	Gly	Thr	Ser	Pro	Leu	Ala	Lys	Ile	485	490	495
Pro	Lys	Ser	Gly	Thr	Ser	Pro	Thr	Pro	Val	Ala	Pro	Asn	Ser	Trp	Ala	500	505	510
Ala	Leu	Arg	Pro	Gln	Gln	Gln	Gln	Gln	Gln	Gln	Gln	Pro	Val	Thr	Glu	515	520	525
Gly	Tyr	Gln	Tyr	Gln	Gln	Thr	Ser	Pro	Ala	Arg	Ser	Pro	Ser	Gly	Pro	530	535	540
Thr	Tyr	Thr	Gln	Leu	Ser	Ala	Gly	Asn	Gly	Asn	Arg	Gln	Gln	Ala	Gln	545	550	555

Pro Gly Ala Tyr Gln Ala Gly Pro Pro Pro Pro Pro Asn Ala Pro Gly
565 570 575

Met Trp Asp Trp Gln Gln Ala Gly Gly His Pro His Pro Pro His Pro
580 585 590

Thr Ala His Pro His His Pro His Ala His Pro Gly Gly Pro Ala Gly
595 600 605

Ala Gly Gln Pro Gln Gly Gln Gly Val Leu Arg Tyr Ala Ala Asp Val
610 615 620

Gly Ser His Ala Asp His Val
625 630

<210> 9

<211> 789

<212> PRT

<213> Homo sapiens

<400> 9

Met Ala Ala Thr Thr Ala Asn Pro Glu Met Thr Ser Asp Val Pro Ser
1 5 10 15

Leu Gly Pro Ala Ile Ala Ser Gly Asn Ser Gly Pro Gly Ile Gln Gly
20 25 30

Gly Gly Ala Ile Val Gln Arg Ala Ile Lys Arg Arg Pro Gly Leu Asp
35 40 45

Phe Asp Asp Asp Gly Glu Gly Asn Ser Lys Phe Leu Arg Cys Asp Asp
50 55 60

Asp Gln Met Ser Asn Asp Lys Glu Arg Phe Ala Arg Ser Asp Asp Glu
65 70 75 80

Gln Ser Ser Ala Asp Lys Glu Arg Leu Ala Arg Glu Asn His Ser Glu
85 90 95

Ile Glu Arg Arg Arg Arg Asn Lys Met Thr Ala Tyr Ile Thr Glu Leu
100 105 110

Ser Asp Met Val Pro Thr Cys Ser Ala Leu Ala Arg Lys Pro Asp Lys
115 120 125

Leu Thr Ile Leu Arg Met Ala Val Ser His Met Lys Ser Leu Arg Gly
130 135 140

Thr Gly Asn Thr Ser Thr Asp Gly Ser Tyr Lys Pro Ser Phe Leu Thr
145 150 155 160

Asp Gln Glu Leu Lys His Leu Ile Leu Glu Ala Ala Asp Gly Phe Leu
165 170 175

Phe Ile Val Ser Cys Glu Thr Gly Arg Val Val Tyr Val Ser Asp Ser
180 185 190

Val	Thr	Pro	Val	Leu	Asn	Gln	Pro	Gln	Ser	Glu	Trp	Phe	Gly	Ser	Thr	195	200	205
Leu	Tyr	Asp	Gln	Val	His	Pro	Asp	Asp	Val	Asp	Lys	Leu	Arg	Glu	Gln	210	215	220
Leu	Ser	Thr	Ser	Glu	Asn	Ala	Leu	Thr	Gly	Arg	Ile	Leu	Asp	Leu	Lys	225	230	240
Thr	Gly	Thr	Val	Lys	Lys	Glu	Gly	Gln	Gln	Ser	Ser	Met	Arg	Met	Cys	245	250	255
Met	Gly	Ser	Arg	Arg	Ser	Phe	Ile	Cys	Arg	Met	Arg	Cys	Gly	Ser	Ser	260	265	270
Ser	Val	Asp	Pro	Val	Ser	Val	Asn	Arg	Leu	Ser	Phe	Val	Arg	Asn	Arg	275	280	285
Cys	Arg	Asn	Gly	Leu	Gly	Ser	Val	Lys	Asp	Gly	Glu	Pro	His	Phe	Val	290	295	300
Val	Val	His	Cys	Thr	Gly	Tyr	Ile	Lys	Ala	Trp	Pro	Pro	Ala	Gly	Val	305	310	315
Ser	Leu	Pro	Asp	Asp	Asp	Pro	Glu	Ala	Gly	Gln	Gly	Ser	Lys	Phe	Cys	325	330	335
Leu	Val	Ala	Ile	Gly	Arg	Leu	Gln	Val	Thr	Ser	Ser	Pro	Asn	Cys	Thr	340	345	350
Asp	Met	Ser	Asn	Val	Cys	Gln	Pro	Thr	Glu	Phe	Ile	Ser	Arg	His	Asn	355	360	365
Ile	Glu	Gly	Ile	Phe	Thr	Phe	Val	Asp	His	Arg	Cys	Val	Ala	Thr	Val	370	375	380
Gly	Tyr	Gln	Pro	Gln	Glu	Leu	Leu	Gly	Lys	Asn	Ile	Val	Glu	Phe	Cys	385	390	395
His	Pro	Glu	Asp	Gln	Gln	Leu	Leu	Arg	Asp	Ser	Phe	Gln	Gln	Val	Val	405	410	415
Lys	Leu	Lys	Gly	Gln	Val	Leu	Ser	Val	Met	Phe	Arg	Phe	Arg	Ser	Lys	420	425	430
Asn	Gln	Glu	Trp	Leu	Trp	Met	Arg	Thr	Ser	Ser	Phe	Thr	Phe	Gln	Asn	435	440	445
Pro	Tyr	Ser	Asp	Glu	Ile	Glu	Tyr	Ile	Ile	Cys	Thr	Asn	Thr	Asn	Val	450	455	460
Lys	Asn	Ser	Ser	Gln	Glu	Pro	Arg	Pro	Thr	Leu	Ser	Asn	Thr	Ile	Gln	465	470	475
Arg	Pro	Gln	Leu	Gly	Pro	Thr	Ala	Asn	Leu	Pro	Leu	Glu	Met	Gly	Ser	485	490	495

Gly Gln Leu Ala Pro Arg Gln Gln Gln Gln Gln Thr Glu Leu Asp Met
 500 505 510
 Val Pro Gly Arg Asp Gly Leu Ala Ser Tyr Asn His Ser Gln Val Val
 515 520 525
 Gln Pro Val Thr Thr Thr Gly Pro Glu His Ser Lys Pro Leu Glu Lys
 530 535 540
 Ser Asp Gly Leu Phe Ala Gln Asp Arg Asp Pro Arg Phe Ser Glu Ile
 545 550 555 560
 Tyr His Asn Ile Asn Ala Asp Gln Ser Lys Gly Ile Ser Ser Ser Thr
 565 570 575
 Val Pro Ala Thr Gln Gln Leu Phe Ser Gln Gly Asn Thr Phe Pro Pro
 580 585 590
 Thr Pro Arg Pro Ala Glu Asn Phe Arg Asn Ser Gly Leu Ala Pro Pro
 595 600 605
 Val Thr Ile Val Gln Pro Ser Ala Ser Ala Gly Gln Met Leu Ala Gln
 610 615 620
 Ile Ser Arg His Ser Asn Pro Thr Gln Gly Ala Thr Pro Thr Trp Thr
 625 630 635 640
 Pro Thr Thr Arg Ser Gly Phe Ser Ala Gln Gln Val Ala Thr Gln Ala
 645 650 655
 Thr Ala Lys Thr Arg Thr Ser Gln Phe Gly Val Gly Ser Phe Gln Thr
 660 665 670
 Pro Ser Ser Phe Ser Ser Met Ser Leu Pro Gly Ala Pro Thr Ala Ser
 675 680 685
 Pro Gly Ala Ala Ala Tyr Pro Ser Leu Thr Asn Arg Gly Ser Asn Phe
 690 695 700
 Ala Pro Glu Thr Gly Gln Thr Ala Gly Gln Phe Gln Thr Arg Thr Ala
 705 710 715 720
 Glu Gly Val Gly Val Trp Pro Gln Trp Gln Gly Gln Gln Pro His His
 725 730 735
 Arg Ser Ser Ser Ser Glu Gln His Val Gln Gln Pro Pro Ala Gln Gln
 740 745 750
 Pro Gly Gln Pro Glu Val Phe Gln Glu Met Leu Ser Met Leu Gly Asp
 755 760 765
 Gln Ser Asn Ser Tyr Asn Asn Glu Glu Phe Pro Asp Leu Thr Met Phe
 770 775 780
 Pro Pro Phe Ser Glu
 785

<210> 10
 <211> 626
 <212> PRT
 <213> Unknown

<220>

<223> Description of Unknown Sequence: Bmall amino acid
 sequence

<400> 10

Met	Ala	Asp	Gln	Arg	Met	Asp	Ile	Ser	Ser	Thr	Ile	Ser	Asp	Phe	Met	1	5	10	15
Ser	Pro	Gly	Pro	Thr	Asp	Leu	Leu	Ser	Ser	Ser	Leu	Gly	Thr	Ser	Gly	20	25	30	
Val	Asp	Cys	Asn	Arg	Lys	Arg	Lys	Gly	Ser	Ser	Thr	Asp	Tyr	Gln	Glu	35	40	45	
Ser	Met	Asp	Thr	Asp	Lys	Asp	Asp	Pro	His	Gly	Arg	Leu	Glu	Tyr	Thr	50	55	60	
Glu	His	Gln	Gly	Arg	Ile	Lys	Asn	Ala	Arg	Glu	Ala	His	Ser	Gln	Ile	65	70	75	80
Glu	Lys	Arg	Arg	Arg	Asp	Lys	Met	Asn	Ser	Phe	Ile	Asp	Glu	Leu	Ala	85	90	95	
Ser	Leu	Val	Pro	Thr	Cys	Asn	Ala	Met	Ser	Arg	Lys	Leu	Asp	Lys	Leu	100	105	110	
Thr	Val	Leu	Arg	Met	Ala	Val	Gln	His	Met	Arg	Thr	Leu	Arg	Gly	Ala	115	120	125	
Thr	Asn	Pro	Tyr	Thr	Glu	Ala	Asn	Tyr	Lys	Pro	Thr	Phe	Leu	Ser	Asp	130	135	140	
Asp	Glu	Leu	Lys	His	Leu	Ile	Leu	Arg	Ala	Ala	Asp	Gly	Phe	Leu	Phe	145	150	155	160
Val	Val	Gly	Cys	Asp	Arg	Gly	Lys	Ile	Leu	Phe	Val	Ser	Glu	Ser	Val	165	170	175	
Phe	Lys	Ile	Leu	Asn	Tyr	Ser	Gln	Asn	Asp	Leu	Ile	Gly	Gln	Ser	Leu	180	185	190	
Phe	Asp	Tyr	Leu	His	Pro	Lys	Asp	Ile	Ala	Lys	Val	Lys	Glu	Gln	Leu	195	200	205	
Ser	Ser	Ser	Asp	Thr	Ala	Pro	Arg	Glu	Arg	Leu	Ile	Asp	Ala	Lys	Thr	210	215	220	
Gly	Leu	Pro	Val	Lys	Thr	Asp	Ile	Thr	Pro	Gly	Pro	Ser	Arg	Leu	Cys	225	230	235	240
Ser	Gly	Ala	Arg	Arg	Ser	Phe	Phe	Cys	Arg	Met	Lys	Cys	Asn	Arg	Pro	245	250	255	

Ser	Val	Lys	Val	Glu	Asp	Lys	Asp	Phe	Pro	Ser	Thr	Cys	Ser	Lys	Lys	260	265	270	
Lys	Ala	Asp	Arg	Lys	Ser	Phe	Cys	Thr	Ile	His	Ser	Thr	Gly	Tyr	Leu	275	280	285	
Lys	Ser	Trp	Pro	Pro	Thr	Lys	Met	Gly	Leu	Asp	Glu	Asp	Asn	Glu	Pro	290	295	300	
Asp	Asn	Glu	Gly	Cys	Asn	Leu	Ser	Cys	Leu	Val	Ala	Ile	Gly	Arg	Leu	305	310	315	320
His	Ser	His	Val	Val	Pro	Gln	Pro	Val	Asn	Gly	Glu	Ile	Arg	Val	Lys	325	330	335	
Ser	Met	Glu	Tyr	Val	Ser	Arg	His	Ala	Ile	Asp	Gly	Lys	Phe	Val	Phe	340	345	350	
Val	Asp	Gln	Arg	Ala	Thr	Ala	Ile	Leu	Ala	Tyr	Leu	Pro	Gln	Glu	Leu	355	360	365	
Leu	Gly	Thr	Ser	Cys	Tyr	Glu	Tyr	Phe	His	Gln	Asp	Asp	Ile	Gly	His	370	375	380	
Leu	Ala	Glu	Cys	His	Arg	Gln	Val	Leu	Gln	Thr	Arg	Glu	Lys	Ile	Thr	385	390	395	400
Thr	Asn	Cys	Tyr	Lys	Phe	Lys	Ile	Lys	Asp	Gly	Ser	Phe	Ile	Thr	Leu	405	410	415	
Arg	Ser	Arg	Trp	Phe	Ser	Phe	Met	Asn	Pro	Trp	Thr	Lys	Glu	Val	Glu	420	425	430	
Tyr	Ile	Val	Ser	Thr	Asn	Thr	Val	Val	Leu	Ala	Asn	Val	Leu	Glu	Gly	435	440	445	
Gly	Asp	Pro	Thr	Phe	Pro	Gln	Leu	Thr	Ala	Ser	Pro	His	Ser	Met	Asp	450	455	460	
Ser	Met	Leu	Pro	Ser	Gly	Glu	Gly	Gly	Pro	Lys	Arg	Thr	His	Pro	Thr	465	470	475	480
Val	Pro	Gly	Ile	Pro	Gly	Gly	Thr	Arg	Ala	Gly	Ala	Gly	Lys	Ile	Gly	485	490	495	
Arg	Met	Ile	Ala	Glu	Glu	Ile	Met	Glu	Ile	His	Arg	Ile	Arg	Gly	Ser	500	505	510	
Ser	Pro	Ser	Ser	Cys	Gly	Ser	Ser	Pro	Leu	Asn	Ile	Thr	Ser	Thr	Pro	515	520	525	
Pro	Pro	Asp	Ala	Ser	Ser	Pro	Gly	Gly	Lys	Lys	Ile	Leu	Asn	Gly	Gly	530	535	540	
Thr	Pro	Asp	Ile	Pro	Ser	Ser	Gly	Leu	Leu	Ser	Gly	Gln	Ala	Gln	Glu	545	550	555	560

Asn Pro Gly Tyr Pro Tyr Ser Asp Ser Ser Ser Ile Leu Gly Glu Asn
565 570 575

Pro His Ile Gly Ile Asp Met Ile Asp Asn Asp Gln Gly Ser Ser Ser
580 585 590

Pro Ser Asn Asp Glu Ala Ala Met Ala Val Ile Met Ser Leu Leu Glu
595 600 605

Ala Asp Ala Gly Leu Gly Gly Pro Val Asp Phe Ser Asp Leu Pro Trp
610 615 620

Pro Leu
625

<210> 11

<211> 716

<212> PRT

<213> Drosophila sp.

<400> 11

Met Ala Ala Pro Glu Thr Gly Asn Thr Gly Ser Thr Gly Ser Ala Gly
1 5 10 15

Ser Thr Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser Ser Ser
20 25 30

Asp Pro Ala Asn Gly Arg Glu Ala Arg Asn Leu Ala Glu Lys Gln Arg
35 40 45

Arg Asp Lys Leu Asn Ala Ser Ile Gln Glu Leu Ala Thr Met Val Pro
50 55 60

His Ala Ala Glu Ser Ser Arg Arg Leu Asp Lys Thr Ala Val Leu Arg
65 70 75 80

Phe Ala Thr His Gly Leu Arg Leu Gln Tyr Val Phe Gly Lys Ser Ala
85 90 95

Ser Arg Arg Arg Lys Lys Pro Gly Leu Lys Gly Thr Gly Met Ser Ala
100 105 110

Ser Pro Val Gly Asp Leu Pro Asn Pro Ser Leu His Leu Thr Asp Thr
115 120 125

Leu Met Gln Leu Leu Asp Cys Cys Phe Leu Thr Leu Thr Cys Ser Gly
130 135 140

Gln Ile Val Leu Val Ser Thr Ser Val Glu Gln Leu Leu Gly His Cys
145 150 155 160

Gln Ser Asp Leu Tyr Gly Gln Asn Leu Leu Gln Ile Thr His Pro Asp
165 170 175

Asp Gln Asp Leu Leu Arg Gln Gln Leu Ile Pro Arg Asp Ile Glu Thr
180 185 190

Leu	Phe	Tyr	Gln	His	Gln	His	His	Gln	Gln	Gln	Gly	His	Asn	Pro	Gln	195	200	205	
Gln	His	Ser	Thr	Ser	Thr	Ser	Ala	Ser	Ala	Ser	Gly	Ser	Asp	Leu	Glu	210	215	220	
Glu	Glu	Glu	Met	Glu	Thr	Glu	Glu	His	Arg	Leu	Gly	Arg	Gln	Gln	Gly	225	230	235	240
Glu	Ala	Asp	Asp	Asp	Glu	Asp	His	Pro	Tyr	Asn	Arg	Arg	Thr	Pro	Ser	245	250	255	
Pro	Arg	Arg	Met	Ala	His	Leu	Ala	Thr	Ile	Asp	Asp	Arg	Leu	Arg	Met	260	265	270	
Asp	Trp	Arg	Cys	Phe	Thr	Val	Arg	Leu	Ala	Arg	Ala	Ser	Thr	Arg	Ala	275	280	285	
Glu	Ala	Thr	Arg	His	Tyr	Glu	Arg	Val	Lys	Ile	Asp	Gly	Cys	Phe	Arg	290	295	300	
Arg	Ser	Asp	Ser	Ser	Leu	Thr	Gly	Gly	Ala	Ala	Ala	Asn	Tyr	Pro	Ile	305	310	315	320
Val	Ser	Gln	Leu	Ile	Arg	Arg	Ser	Arg	Asn	Asn	Asn	Met	Leu	Ala	Ala	325	330	335	
Ala	Ala	Ala	Val	Ala	Ala	Glu	Ala	Ala	Thr	Val	Pro	Pro	Gln	His	Asp	340	345	350	
Ala	Ile	Ala	Gln	Ala	Ala	Leu	His	Gly	Ile	Ser	Gly	Asn	Asp	Ile	Val	355	360	365	
Leu	Val	Ala	Met	Ala	Arg	Val	Leu	Arg	Glu	Glu	Arg	Pro	Pro	Glu	Glu	370	375	380	
Thr	Glu	Gly	Thr	Val	Gly	Leu	Thr	Ile	Tyr	Arg	Gln	Pro	Glu	Pro	Tyr	385	390	395	400
Gln	Leu	Glu	Tyr	His	Thr	Arg	His	Leu	Ile	Asp	Gly	Ser	Ile	Ile	Asp	405	410	415	
Cys	Asp	Gln	Arg	Ile	Gly	Leu	Val	Ala	Gly	Tyr	Met	Lys	Asp	Glu	Val	420	425	430	
Arg	Asn	Leu	Ser	Pro	Phe	Cys	Phe	Met	His	Leu	Asp	Asp	Val	Arg	Trp	435	440	445	
Val	Ile	Val	Ala	Leu	Arg	Gln	Met	Tyr	Asp	Cys	Asn	Ser	Asp	Tyr	Gly	450	455	460	
Glu	Ser	Cys	Tyr	Arg	Leu	Leu	Ser	Arg	Asn	Gly	Arg	Phe	Ile	Tyr	Leu	465	470	475	480
His	Thr	Lys	Gly	Phe	Leu	Glu	Val	Asp	Arg	Gly	Ser	Asn	Lys	Val	His	485	490	495	

Ser Phe Leu Cys Val Asn Thr Leu Leu Asp Glu Glu Ala Gly Arg Gln
 500 505 510
 Lys Val Gln Glu Met Lys Glu Lys Phe Ser Thr Ile Ile Lys Ala Glu
 515 520 525
 Met Pro Thr Gln Ser Ser Ser Pro Asp Leu Pro Ala Ser Gln Ala Pro
 530 535 540
 Gln Gln Leu Glu Arg Ile Val Leu Tyr Leu Ile Glu Asn Leu Gln Lys
 545 550 555 560
 Ser Val Asp Ser Ala Glu Thr Val Gly Gly Gln Gly Met Glu Ser Leu
 565 570 575
 Met Asp Asp Gly Tyr Ser Ser Pro Ala Asn Thr Leu Thr Leu Glu Glu
 580 585 590
 Leu Ala Pro Ser Pro Thr Pro Ala Leu Ala Leu Val Pro Pro Ala Pro
 595 600 605
 Ser Ser Val Lys Ser Ser Ile Ser Lys Ser Val Ser Val Val Asn Val
 610 615 620
 Thr Ala Ala Arg Lys Phe Gln Gln Glu His Gln Lys Gln Arg Glu Arg
 625 630 635 640
 Asp Arg Glu Gln Leu Lys Glu Arg Thr Asn Ser Thr Gln Gly Val Ile
 645 650 655
 Arg Gln Leu Ser Ser Cys Leu Ser Glu Ala Glu Thr Ala Ser Cys Ile
 660 665 670
 Leu Ser Pro Ala Ser Ser Leu Ser Ala Ser Glu Ala Pro Asp Thr Pro
 675 680 685
 Asp Pro His Ser Asn Thr Ser Pro Pro Pro Ser Leu His Thr Arg Pro
 690 695 700
 Ser Val Leu His Arg Thr Leu Thr Ser Thr Leu Arg
 705 710 715

<210> 12

<211> 808

<212> PRT

<213> Homo sapiens

<400> 12

Met Asn Ser Ser Ser Ala Asn Ile Thr Tyr Ala Ser Arg Lys Arg Arg
 1 5 10 15
 Lys Pro Val Gln Lys Thr Val Lys Pro Ile Pro Ala Glu Gly Ile Lys
 20 25 30
 Ser Asn Pro Ser Lys Arg His Arg Asp Arg Leu Asn Thr Glu Leu Asp
 35 40 45

Arg Leu Ala Ser Leu Leu Pro Phe Pro Gln Asp Val Ile Asn Lys Leu
 50 55 60
 Asp Lys Leu Ser Val Leu Arg Leu Ser Val Ser Tyr Leu Arg Ala Lys
 65 70 75 80
 Ser Phe Phe Asp Val Ala Leu Lys Ser Ser Pro Thr Glu Arg Asn Gly
 85 90 95
 Gly Gln Asp Asn Cys Arg Ala Ala Asn Phe Arg Glu Gly Leu Asn Leu
 100 105 110
 Gln Glu Gly Glu Phe Leu Leu Gln Ala Leu Asn Gly Phe Val Leu Val
 115 120 125
 Val Thr Thr Asp Ala Leu Val Phe Tyr Ala Ser Ser Thr Ile Gln Asp
 130 135 140
 Tyr Leu Gly Phe Gln Gln Ser Asp Val Ile His Gln Ser Val Tyr Glu
 145 150 155 160
 Leu Ile His Thr Glu Asp Arg Ala Glu Phe Gln Arg Gln Leu His Trp
 165 170 175
 Ala Leu Asn Pro Ser Gln Cys Thr Glu Ser Gly Gln Gly Ile Glu Glu
 180 185 190
 Ala Thr Gly Leu Pro Gln Thr Val Val Cys Tyr Asn Pro Asp Gln Ile
 195 200 205
 Pro Pro Glu Asn Ser Pro Leu Met Glu Arg Cys Phe Ile Cys Arg Leu
 210 215 220
 Arg Cys Leu Leu Asp Asn Ser Ser Gly Phe Leu Ala Met Asn Phe Gln
 225 230 235 240
 Gly Lys Leu Lys Tyr Leu His Gly Gln Lys Lys Lys Gly Lys Asp Gly
 245 250 255
 Ser Ile Leu Pro Pro Gln Leu Ala Leu Phe Ala Ile Ala Thr Pro Leu
 260 265 270
 Gln Pro Pro Ser Ile Leu Glu Ile Arg Thr Lys Asn Phe Ile Phe Arg
 275 280 285
 Thr Lys His Lys Leu Asp Phe Thr Pro Ile Gly Cys Asp Ala Lys Gly
 290 295 300
 Arg Ile Val Leu Gly Tyr Thr Glu Ala Glu Leu Cys Thr Arg Gly Ser
 305 310 315 320
 Gly Tyr Gln Phe Ile His Ala Ala Asp Met Leu Tyr Cys Ala Glu Ser
 325 330 335
 His Ile Arg Met Ile Lys Thr Gly Glu Ser Gly Met Ile Val Phe Arg
 340 345 350

Leu Leu Thr Lys Asn Asn Arg Trp Thr Trp Val Gln Ser Asn Ala Arg
 355 360 365
 Leu Leu Tyr Lys Asn Gly Arg Pro Asp Tyr Ile Ile Val Thr Gln Arg
 370 375 380
 Pro Leu Thr Asp Glu Glu Gly Thr Glu His Leu Arg Lys Arg Asn Thr
 385 390 395 400
 Lys Leu Pro Phe Met Phe Thr Thr Gly Glu Ala Val Leu Tyr Glu Ala
 405 410 415
 Thr Asn Pro Phe Pro Ala Ile Met Asp Pro Leu Pro Leu Arg Thr Lys
 420 425 430
 Asn Gly Thr Ser Gly Lys Asp Ser Ala Thr Thr Ser Thr Leu Ser Lys
 435 440 445
 Asp Ser Leu Asn Pro Ser Ser Leu Leu Ala Ala Met Met Gln Gln Asp
 450 455 460
 Glu Ser Ile Tyr Leu Tyr Pro Ala Ser Ser Thr Ser Ser Thr Ala Pro
 465 470 475 480
 Phe Glu Asn Asn Phe Phe Asn Glu Ser Met Asn Glu Cys Arg Asn Trp
 485 490 495
 Gln Asp Asn Thr Ala Pro Met Gly Asn Asp Thr Ile Leu Lys His Glu
 500 505 510
 Gln Ile Asp Gln Pro Gln Asp Val Asn Ser Phe Ala Gly Gly His Pro
 515 520 525
 Gly Leu Phe Gln Asp Ser Lys Asn Ser Asp Leu Tyr Ser Ile Met Lys
 530 535 540
 Asn Leu Gly Ile Asp Phe Glu Asp Ile Arg His Met Gln Asn Glu Lys
 545 550 555 560
 Phe Phe Arg Asn Asp Phe Ser Gly Glu Val Asp Phe Arg Asp Ile Asp
 565 570 575
 Leu Thr Asp Glu Ile Leu Thr Tyr Val Gln Asp Ser Leu Ser Lys Ser
 580 585 590
 Pro Phe Ile Pro Ser Asp Tyr Gln Gln Gln Gln Ser Leu Ala Leu Asn
 595 600 605
 Ser Ser Cys Met Val Gln Glu His Leu His Leu Glu Gln Gln Gln Gln
 610 615 620
 His His Gln Lys Gln Val Val Val Glu Pro Gln Gln Gln Leu Cys Gln
 625 630 635 640
 Lys Met Lys His Met Gln Val Asn Gly Met Phe Glu Asn Trp Asn Ser
 645 650 655

Asn Gln Phe Val Pro Phe Asn Cys Pro Gln Gln Asp Pro Gln Gln Tyr
 660 665 670

Asn Val Phe Thr Asp Leu His Gly Ile Ser Gln Glu Phe Pro Tyr Lys
 675 680 685

Ser Glu Met Asp Ser Met Pro Tyr Thr Gln Asn Phe Ile Ser Cys Asn
 690 695 700

Gln Pro Val Leu Pro Gln His Ser Lys Cys Thr Glu Leu Asp Tyr Pro
 705 710 715 720

Met Gly Ser Phe Glu Pro Ser Pro Tyr Pro Thr Thr Ser Ser Leu Glu
 725 730 735

Asp Phe Val Thr Cys Leu Gln Leu Pro Glu Asn Gln Lys His Gly Leu
 740 745 750

Asn Pro Gln Ser Ala Ile Ile Thr Pro Gln Thr Cys Tyr Ala Gly Ala
 755 760 765

Val Ser Met Tyr Gln Cys Gln Pro Glu Pro Gln His Thr His Val Gly
 770 775 780

Gln Met Gln Tyr Asn Pro Val Leu Pro Gly Gln Gln Ala Phe Leu Asn
 785 790 795 800

Lys Phe Gln Asn Gly Val Phe Lys
 805

<210> 13

<211> 10

<212> DNA

<213> Drosophila sp.

<400> 13

caaaatggca